RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _09/725, 019A_

Source: _____

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           RAW SEQUENCE LISTING                    DATE: 12/23/2004
           PATENT APPLICATION:  US/09/725,019A     TIME: 14:34:23

           Input Set : N:\Crf3\RULE60\09725019a.raw.txt
           Output Set: N:\CRF4\12232004\I725019A.raw
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 1  <110> APPLICANT: Thompson, John E.
 2         Wang, Tzann-Wei
 3         Lu, Dongen Lilly
 4  <120> TITLE OF INVENTION: DNA ENCODING A PLANT DEOXYHYPUSINE SYNTHASE, TRANSGENIC
 5         PLANTS AND A METHOD FOR CONTROLLING PROGRAMMED CELL
 6         DEATH IN PLANTS
 7  <130> FILE REFERENCE: 10799/9
 8  <140> CURRENT APPLICATION NUMBER: US/09/725,019A
 9  <141> CURRENT FILING DATE: 2000-11-29
10  <150> PRIOR APPLICATION NUMBER: US/09/597,771
11  <151> PRIOR FILING DATE: 2000-06-19
12  <150> PRIOR APPLICATION NUMBER: 09/348,675
13  <151> PRIOR FILING DATE: 1999-07-06
14  <160> NUMBER OF SEQ ID NOS: 35
15  <170> SOFTWARE: PatentIn Ver. 2.1
17  <210> SEQ ID NO: 1
18  <211> LENGTH: 1609
19  <212> TYPE: DNA
20  <213> ORGANISM: Lycopersicon sp.
21  <220> FEATURE:
22  <221> NAME/KEY: CDS
23  <222> LOCATION: (54..1196)
24  <220> FEATURE:
25  <223> OTHER INFORMATION: DHS
26  <400> SEQUENCE: 1
27        cgcagaaact cgcggcggca gtcttgttcc ctacataatc ttggtctgca ata atg        56
28                                                                      Met
29                                                                       1
30        gga gaa gct ctg aag tac agt atc atg gac tca gta aga tcg gta gtt      104
31        Gly Glu Ala Leu Lys Tyr Ser Ile Met Asp Ser Val Arg Ser Val Val
32                        5                   10                  15
33        ttc aaa gaa tcc gaa aat cta gaa ggt tct tgc act aaa atc gag ggc      152
34        Phe Lys Glu Ser Glu Asn Leu Glu Gly Ser Cys Thr Lys Ile Glu Gly
35                    20                  25                  30
36        tac gac ttc aat aaa ggc gtt aac tat gct gag ctg atc aag tcc atg      200
37        Tyr Asp Phe Asn Lys Gly Val Asn Tyr Ala Glu Leu Ile Lys Ser Met
38              35                  40                  45
39        gtt tcc act ggt ttc caa gca tct aat ctt ggt gac gcc att gca att      248
40        Val Ser Thr Gly Phe Gln Ala Ser Asn Leu Gly Asp Ala Ile Ala Ile
41         50                  55                  60                  65
42        gtt aat caa atg cta gat tgg agg ctt tca cat gag ctg ccc acg gag      296
43        Val Asn Gln Met Leu Asp Trp Arg Leu Ser His Glu Leu Pro Thr Glu
44                        70                  75                  80
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45        gat tgc agt gaa gaa gaa aga gat gtt gca tac aga gag tcg gta acc        344
46        Asp Cys Ser Glu Glu Glu Arg Asp Val Ala Tyr Arg Glu Ser Val Thr
47                    85                  90                  95
48        tgc aaa atc ttc ttg ggg ttc act tca aac ctt gtt tct tct ggt gtt        392
49        Cys Lys Ile Phe Leu Gly Phe Thr Ser Asn Leu Val Ser Ser Gly Val
50                    100                 105                 110
51        aga gac act gtc cgc tac ctt gtt cag cac cgg atg gtt gat gtt gtg        440
52        Arg Asp Thr Val Arg Tyr Leu Val Gln His Arg Met Val Asp Val Val
53                    115                 120                 125
54        gtt act aca gct ggt ggt att gaa gag gat ctc ata aag tgc ctc gca        488
55        Val Thr Thr Ala Gly Gly Ile Glu Glu Asp Leu Ile Lys Cys Leu Ala
56        130                 135                 140                 145
57        cca acc tac aag ggg gac ttc tct tta cct gga gct tct cta cga tcg        536
58        Pro Thr Tyr Lys Gly Asp Phe Ser Leu Pro Gly Ala Ser Leu Arg Ser
59                    150                 155                 160
60        aaa gga ttg aac cgt att ggt aac tta ttg gtt cct aat gac aac tac        584
61        Lys Gly Leu Asn Arg Ile Gly Asn Leu Leu Val Pro Asn Asp Asn Tyr
62                    165                 170                 175
63        tgc aaa ttt gag aat tgg atc atc cca gtt ttt gac caa atg tat gag        632
64        Cys Lys Phe Glu Asn Trp Ile Ile Pro Val Phe Asp Gln Met Tyr Glu
65                    180                 185                 190
66        gag cag att aat gag aag gtt cta tgg aca cca tct aaa gtc att gct        680
67        Glu Gln Ile Asn Glu Lys Val Leu Trp Thr Pro Ser Lys Val Ile Ala
68                    195                 200                 205
69        cgt ctg ggt aaa gaa att aat gat gaa acc tca tac ttg tat tgg gct        728
70        Arg Leu Gly Lys Glu Ile Asn Asp Glu Thr Ser Tyr Leu Tyr Trp Ala
71        210                 215                 220                 225
72        tac aag aac cgg att cct gtc ttc tgt cct ggc ttg acg gat gga tca        776
73        Tyr Lys Asn Arg Ile Pro Val Phe Cys Pro Gly Leu Thr Asp Gly Ser
74                    230                 235                 240
75        ctt ggt gac atg cta tac ttc cat tct ttc aaa aag ggt gat cca gat        824
76        Leu Gly Asp Met Leu Tyr Phe His Ser Phe Lys Lys Gly Asp Pro Asp
77                    245                 250                 255
78        aat cca gat ctt aat cct ggt cta gtc ata gac att gta gga gat att        872
79        Asn Pro Asp Leu Asn Pro Gly Leu Val Ile Asp Ile Val Gly Asp Ile
80                    260                 265                 270
81        agg gcc atg aat ggt gaa gct gtc cat gct ggt ttg agg aag aca gga        920
82        Arg Ala Met Asn Gly Glu Ala Val His Ala Gly Leu Arg Lys Thr Gly
83                    275                 280                 285
84        atg att ata ctg ggt gga ggg ctg cct aag cac cat gtt tgc aat gcc        968
85        Met Ile Ile Leu Gly Gly Gly Leu Pro Lys His His Val Cys Asn Ala
86        290                 295                 300                 305
87        aat atg atg cgc aat ggt gca gat ttt gcc gtc ttc att aac acc gca        1016
88        Asn Met Met Arg Asn Gly Ala Asp Phe Ala Val Phe Ile Asn Thr Ala
89                    310                 315                 320
90        caa gag ttt gat ggt agt gac tct ggt gcc cgt cct gat gaa gct gta        1064
91        Gln Glu Phe Asp Gly Ser Asp Ser Gly Ala Arg Pro Asp Glu Ala Val
92                    325                 330                 335
93        tca tgg gga aag ata cgt ggt ggt gcc aag act gtg aag gtg cat tgt        1112
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94        Ser Trp Gly Lys Ile Arg Gly Gly Ala Lys Thr Val Lys Val His Cys
95            340             345             350
96        gat gca acc att gca ttt ccc ata tta gta gct gag aca ttt gca gct       1160
97        Asp Ala Thr Ile Ala Phe Pro Ile Leu Val Ala Glu Thr Phe Ala Ala
98            355             360             365
99        aag agt aag gaa ttc tcc cag ata agg tgc caa gtt tgaacattga            1206
100       Lys Ser Lys Glu Phe Ser Gln Ile Arg Cys Gln Val
101       370             375             380
102       ggaagctgtc cttccgacca cacatatgaa ttgctagctt ttgaagccaa cttgctagtg       1266
103       tgcagcacca tttattctgc aaaactgact agagagcagg gtatattcct ctaccccgag       1326
104       ttagacgaca tcctgtatgg ttcaaattaa ttattttct ccccttcaca ccatgttatt       1386
105       tagttctctt cctcttcgaa agtgaagagc ttagatgttc ataggttttg aattatgttg       1446
106       gaggttggtg ataactgact agtcctctta ccatatagat aatgtatcct tgtactatga       1506
107       gattttgggt gtgtttgata ccaaggaaaa tgtttatttg gaaacaatt ggattttttaa      1566
108       tttatttttt cttgtttaaa aaaaaaaaa aaaaaaaaa aaa                          1609
110  <210> SEQ ID NO: 2
111  <211> LENGTH: 381
112  <212> TYPE: PRT
113  <213> ORGANISM: Lycopersicon sp.
114  <220> FEATURE:
115  <223> OTHER INFORMATION: DHS
116  <400> SEQUENCE: 2
117       Met Gly Glu Ala Leu Lys Tyr Ser Ile Met Asp Ser Val Arg Ser Val
118       1               5               10              15
119       Val Phe Lys Glu Ser Glu Asn Leu Glu Gly Ser Cys Thr Lys Ile Glu
120                       20              25              30
121       Gly Tyr Asp Phe Asn Lys Gly Val Asn Tyr Ala Glu Leu Ile Lys Ser
122                   35              40              45
123       Met Val Ser Thr Gly Phe Gln Ala Ser Asn Leu Gly Asp Ala Ile Ala
124           50              55              60
125       Ile Val Asn Gln Met Leu Asp Trp Arg Leu Ser His Glu Leu Pro Thr
126       65              70              75              80
127       Glu Asp Cys Ser Glu Glu Glu Arg Asp Val Ala Tyr Arg Glu Ser Val
128                       85              90              95
129       Thr Cys Lys Ile Phe Leu Gly Phe Thr Ser Asn Leu Val Ser Ser Gly
130                   100             105             110
131       Val Arg Asp Thr Val Arg Tyr Leu Val Gln His Arg Met Val Asp Val
132               115             120             125
133       Val Val Thr Thr Ala Gly Gly Ile Glu Glu Asp Leu Ile Lys Cys Leu
134           130             135             140
135       Ala Pro Thr Tyr Lys Gly Asp Phe Ser Leu Pro Gly Ala Ser Leu Arg
136       145             150             155             160
137       Ser Lys Gly Leu Asn Arg Ile Gly Asn Leu Leu Val Pro Asn Asp Asn
138                   165             170             175
139       Tyr Cys Lys Phe Glu Asn Trp Ile Ile Pro Val Phe Asp Gln Met Tyr
140                   180             185             190
141       Glu Glu Gln Ile Asn Glu Lys Val Leu Trp Thr Pro Ser Lys Val Ile
142               195             200             205
143       Ala Arg Leu Gly Lys Glu Ile Asn Asp Glu Thr Ser Tyr Leu Tyr Trp
```

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144         210                 215                 220
145     Ala Tyr Lys Asn Arg Ile Pro Val Phe Cys Pro Gly Leu Thr Asp Gly
146     225                 230                 235                 240
147     Ser Leu Gly Asp Met Leu Tyr Phe His Ser Phe Lys Lys Gly Asp Pro
148                     245                 250                 255
149     Asp Asn Pro Asp Leu Asn Pro Gly Leu Val Ile Asp Ile Val Gly Asp
150                 260                 265                 270
151     Ile Arg Ala Met Asn Gly Glu Ala Val His Ala Gly Leu Arg Lys Thr
152             275                 280                 285
153     Gly Met Ile Ile Leu Gly Gly Gly Leu Pro Lys His His Val Cys Asn
154         290                 295                 300
155     Ala Asn Met Met Arg Asn Gly Ala Asp Phe Ala Val Phe Ile Asn Thr
156     305                 310                 315                 320
157     Ala Gln Glu Phe Asp Gly Ser Asp Ser Gly Ala Arg Pro Asp Glu Ala
158                     325                 330                 335
159     Val Ser Trp Gly Lys Ile Arg Gly Gly Ala Lys Thr Val Lys Val His
160                 340                 345                 350
161     Cys Asp Ala Thr Ile Ala Phe Pro Ile Leu Val Ala Glu Thr Phe Ala
162             355                 360                 365
163     Ala Lys Ser Lys Glu Phe Ser Gln Ile Arg Cys Gln Val
164         370                 375                 380
166 <210> SEQ ID NO: 3
167 <211> LENGTH: 24
168 <212> TYPE: DNA
169 <213> ORGANISM: Artificial Sequence
170 <220> FEATURE:
171 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
172 <400> SEQUENCE: 3
173     agtctagaag gtgctcgtcc tgat                                       24
175 <210> SEQ ID NO: 4
176 <211> LENGTH: 34
177 <212> TYPE: DNA
178 <213> ORGANISM: Artificial Sequence
179 <220> FEATURE:
180 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
181 <400> SEQUENCE: 4
182     gactgcagtc gacatcgatt tttttttttt tttt                           34
184 <210> SEQ ID NO: 5
185 <211> LENGTH: 2272
186 <212> TYPE: DNA
187 <213> ORGANISM: Arabidopsis sp.
188 <220> FEATURE:
189 <221> NAME/KEY: CDS
190 <222> LOCATION: (68..265, 348..536, 624..842, 979..1065,
191     1154..1258, 1575..1862)
192 <400> SEQUENCE: 5
193     gaactcccaa aaccctctac tactacactt tcagatccaa ggaaatcaat tttgtcattc    60
194     gagcaac atg gag gat gat cgt gtt ttc tct tcg gtt cac tca aca gtt   109
195             Met Glu Asp Asp Arg Val Phe Ser Ser Val His Ser Thr Val
```

```
196                  1               5                    10
197     ttc aaa gaa tcc gaa tca ttg gaa gga aag tgt gat aaa atc gaa gga      157
198     Phe Lys Glu Ser Glu Ser Leu Glu Gly Lys Cys Asp Lys Ile Glu Gly
199      15                  20                  25                  30
200     tac gat ttc aat caa gga gta gat tac cca aag ctt atg cga tcc atg      205
201     Tyr Asp Phe Asn Gln Gly Val Asp Tyr Pro Lys Leu Met Arg Ser Met
202                      35                  40                  45
203     ctc acc acc gga ttt caa gcc tcg aat ctc ggc gaa gct att gat gtc      253
204     Leu Thr Thr Gly Phe Gln Ala Ser Asn Leu Gly Glu Ala Ile Asp Val
205                      50                  55                  60
206     gtc aat caa atg gttcgtttct cgaattcatc aaaaataaaa attccttctt          305
207     Val Asn Gln Met
208                      65
209     tttgttttcc tttgttttgg gtgaattagt aatgacaaag ag ttt gaa ttt gta       359
210                                                        Phe Glu Phe Val
211                                                                     70
212     ttg aag cta gat tgg aga ctg gct gat gaa act aca gta gct gaa gac      407
213     Leu Lys Leu Asp Trp Arg Leu Ala Asp Glu Thr Thr Val Ala Glu Asp
214                      75                  80                  85
215     tgt agt gaa gag gag aag aat cca tcg ttt aga gag tct gtc aag tgt      455
216     Cys Ser Glu Glu Glu Lys Asn Pro Ser Phe Arg Glu Ser Val Lys Cys
217                      90                  95                  100
218     aaa atc ttt cta ggt ttc act tca aat ctt gtt tca tct ggt gtt aga      503
219     Lys Ile Phe Leu Gly Phe Thr Ser Asn Leu Val Ser Ser Gly Val Arg
220                      105                 110                 115
221     gat act att cgt tat ctt gtt cag cat cat atg gtttgtgatt tttgctttat    556
222     Asp Thr Ile Arg Tyr Leu Val Gln His His Met
223          120                 125
224     caccctgctt ttttatagat gttaaaattt tcgagcttta gttttgattt caatggtttt   616
225     tctgcag gtt gat gtt ata gtc acg aca act ggt ggt gtt gag gaa gat      665
226             Val Asp Val Ile Val Thr Thr Thr Gly Gly Val Glu Glu Asp
227             130                 135                 140
228     ctc ata aaa tgc ctt gca cct aca ttt aaa ggt gat ttc tct cta cct      713
229     Leu Ile Lys Cys Leu Ala Pro Thr Phe Lys Gly Asp Phe Ser Leu Pro
230          145                 150                 155
231     gga gct tat tta agg tca aag gga ttg aac cga att ggg aat ttg ctg      761
232     Gly Ala Tyr Leu Arg Ser Lys Gly Leu Asn Arg Ile Gly Asn Leu Leu
233     160                 165                 170                 175
234     gtt cct aat gat aac tac tgc aag ttt gag gat tgg atc att ccc atc      809
235     Val Pro Asn Asp Asn Tyr Cys Lys Phe Glu Asp Trp Ile Ile Pro Ile
236                      180                 185                 190
237     ttt gac gag atg ttg aag gaa cag aaa gaa gag gtattgcttt atctttcctt    862
238     Phe Asp Glu Met Leu Lys Glu Gln Lys Glu Glu
239                      195                 200
240     tttatatgat ttgagatgat tctgtttgtg cgtcactagt ggagatagat tttgattcct   922
241     ctcttgcatc attgacttcg ttggtgaatc cttctttctc tggtttttcc ttgtag       978
242     aat gtg ttg tgg act cct tct aaa ctg tta gca cgg ctg gga aaa gaa     1026
243     Asn Val Leu Trp Thr Pro Ser Lys Leu Leu Ala Arg Leu Gly Lys Glu
244          205                 210                 215
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 12/23/2004
PATENT APPLICATION: US/09/725,019A   TIME: 14:34:24

Input Set : N:\Crf3\RULE60\09725019a.raw.txt
Output Set: N:\CRF4\12232004\I725019A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:19; N Pos. 6
Seq#:31; N Pos. 542

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 4

VARIABLE LOCATION SUMMARY   DATE: 12/23/2004
PATENT APPLICATION: US/09/725,019A   TIME: 14:34:24

Input Set : **N:\Crf3\RULE60\09725019a.raw.txt**
Output Set: **N:\CRF4\12232004\I725019A.raw**

<u>Use of n's or Xaa's(NEW RULES):</u>
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
in <220> to <223> section, please explain location of n or Xaa, and which
residue n or Xaa represents.

Seq#:19; N Pos. 6
Seq#:31; N Pos. 542

VERIFICATION SUMMARY   DATE: 12/23/2004
PATENT APPLICATION: US/09/725,019A   TIME: 14:34:24

        Input Set : **N:\Crf3\RULE60\09725019a.raw.txt**
        Output Set: **N:\CRF4\12232004\I725019A.raw**

L:764 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:19
L:764 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:19
L:764 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0
L:986 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:496